



SEQUENCE LISTING

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<120> MAMMALIAN SUBTILISIN/KEXIN ISOZYME SKI-1: A PROPROTEIN
CONVERTASE WITH A UNIQUE CLEAVAGE SPECIFICITY

<130> IRCM

<140> PCT/CA99/01058

<141> 1999-11-04

<150> CA 2,249,648

<151> 1998-11-04

<160> 76

<170> PatentIn Ver. 2.1

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 Ser Thr Val Val Glu Tyr Glu Tyr Ile Val Ala Phe Asn Gly Tyr Phe
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Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Pro Arg Gln
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His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn Trp Thr Asn Glu
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Lys Val Trp Glu Leu Thr Ala Asn Asn Val Ile Met Val Ser Ala Ile
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Gly Asn Asp Gly Pro Leu Tyr Gly Thr Leu Asn Asn Pro Ala Asp Gln
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Gly Arg Val Lys Pro Asp Ile Val Thr Tyr Gly Ala Gly Val Arg Gly
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Ser Gly Val Lys Gly Gly Cys Arg Ala Leu Ser Gly Thr Ser Val Ala
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Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val Ser Thr Val Gln
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Ser Ala Arg Arg Leu Pro Gly Val Asn Met Phe Glu Gln Gly His Gly
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Gln Ala Ser Leu Ser Pro Ser Tyr Ile Asp Leu Thr Glu Cys Pro Tyr
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Cys	Leu	Asp	Asp	Ser	His	Arg	Gln	Lys	Asp	Cys	Phe	Trp	Leu	Leu	Asp	850	855	860
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His	Ser	Gly	Asn	Arg	Gln	Arg	Pro	Pro	Ser	Gly	Ala	Gly	Leu	Ala	Pro	885	890	895
Pro	Glu	Arg	Met	Glu	Gly	Asn	His	Leu	His	Arg	Tyr	Ser	Lys	Val	Leu	900	905	910
Glu	Ala	His	Leu	Gly	Asp	Pro	Lys	Pro	Arg	Pro	Leu	Pro	Ala	Cys	Pro	915	920	925

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 Val Leu Pro Asn Phe Arg Ser Asn Arg Pro Gln Val Arg Pro Leu Ser
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Asp Asn Ile Ala Arg Phe Ser Ser Arg Gly Met Thr Thr Trp Glu Leu	
365 370 375 380	
cca gga ggc tac ggt cgc atg aaa cct gac att gtc acc tat ggt gct	1684
Pro Gly Gly Tyr Gly Arg Met Lys Pro Asp Ile Val Thr Tyr Gly Ala	
385 390 395	
ggc gtg cgg ggt tct ggc gtg aaa ggg ggg tgc cgg gcc ctc tca ggg	1732
Gly Val Arg Gly Ser Gly Val Lys Gly Gly Cys Arg Ala Leu Ser Gly	
400 405 410	
acc agt gtt gct tct cca gtg gtt gca ggt gct gtc acc ttg tta gtg	1780
Thr Ser Val Ala Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val	
415 420 425	
agc aca gtc cag aag cgt gag ctg gtg aat ccc gcc agt atg aag cag	1828
Ser Thr Val Gln Lys Arg Glu Leu Val Asn Pro Ala Ser Met Lys Gln	
430 435 440	
gcc ctg atc gcg tca gcc cgg agg ctc ccc ggg gtc aac atg ttt gag	1876
Ala Leu Ile Ala Ser Ala Arg Arg Leu Pro Gly Val Asn Met Phe Glu	
445 450 455 460	
caa ggc cac ggc aag ctc gat ctg ctc aga gcc tat cag atc ctc aac	1924
Gln Gly His Gly Lys Leu Asp Leu Leu Arg Ala Tyr Gln Ile Leu Asn	
465 470 475	
agc tac aag cca cag gca agt ttg agc ccc agc tac ata gat ctg act	1972
Ser Tyr Lys Pro Gln Ala Ser Leu Ser Pro Ser Tyr Ile Asp Leu Thr	
480 485 490	
gag tgt ccc tac atg tgg ccc tac tgc tcc cag ccc atc tac tat gga	2020
Glu Cys Pro Tyr Met Trp Pro Tyr Cys Ser Gln Pro Ile Tyr Tyr Gly	
495 500 505	
gga atg ccg aca gtt gtt aat gtc acc atc ctc aac ggc atg gga gtc	2068
Gly Met Pro Thr Val Val Asn Val Thr Ile Leu Asn Gly Met Gly Val	
510 515 520	
aca gga aga att gta gat aag cct gac tgg cag ccc tat ttg cca cag	2116
Thr Gly Arg Ile Val Asp Lys Pro Asp Trp Gln Pro Tyr Leu Pro Gln	
525 530 535 540	
aac gga gac aac att gaa gtt gcc ttc tcc tac tcc tcg gtc tta tgg	2164
Asn Gly Asp Asn Ile Glu Val Ala Phe Ser Tyr Ser Ser Val Leu Trp	
545 550 555	

cct tgg tcg ggc tac ctg gcc atc tcc att tct gtg acc aag aaa gcg	2212
Pro Trp Ser Gly Tyr Leu Ala Ile Ser Ile Ser Val Thr Lys Lys Ala	
560 565 570	
gct tcc tgg gaa ggc att gct cag ggc cat gtc atg atc act gtg gct	2260
Ala Ser Trp Glu Gly Ile Ala Gln Gly His Val Met Ile Thr Val Ala	
575 580 585	
tcc cca gca gag aca gag tca aaa aat ggt gca gaa cag act tca aca	2308
Ser Pro Ala Glu Thr Glu Ser Lys Asn Gly Ala Glu Gln Thr Ser Thr	
590 595 600	
gta aag ctc ccc att aag gtg aag ata att cct act ccc ccg cga agc	2356
Val Lys Leu Pro Ile Lys Val Lys Ile Ile Pro Thr Pro Pro Arg Ser	
605 610 615 620	
aag aga gtt ctc tgg gat cag tac cac aac ctc cgc tat cca cct ggc	2404
Lys Arg Val Leu Trp Asp Gln Tyr His Asn Leu Arg Tyr Pro Pro Gly	
625 630 635	
tat ttc ccc agg gat aat tta agg atg aag aat gac cct tta gac tgg	2452
Tyr Phe Pro Arg Asp Asn Leu Arg Met Lys Asn Asp Pro Leu Asp Trp	
640 645 650	
aat ggt gat cac atc cac acc aat ttc agg gat atg tac cag cat ctg	2500
Asn Gly Asp His Ile His Thr Asn Phe Arg Asp Met Tyr Gln His Leu	
655 660 665	
aga agc atg ggc tac ttt gta gag gtc ctc ggg gcc ccc ttc acg tgt	2548
Arg Ser Met Gly Tyr Phe Val Glu Val Leu Gly Ala Pro Phe Thr Cys	
670 675 680	
ttt gat gcc agt cag tat ggc act ttg ctg atg gtg gac agt gag gag	2596
Phe Asp Ala Ser Gln Tyr Gly Thr Leu Leu Met Val Asp Ser Glu Glu	
685 690 695 700	
gag tac ttc cct gaa gag atc gcc aag ctc cgg agg gac gtg gac aac	2644
Glu Tyr Phe Pro Glu Glu Ile Ala Lys Leu Arg Arg Asp Val Asp Asn	
705 710 715	
ggc ctc tcg ctc gtc atc ttc agt gac tgg tac aac act tct gtt atg	2692
Gly Leu Ser Leu Val Ile Phe Ser Asp Trp Tyr Asn Thr Ser Val Met	
720 725 730	
aga aaa gtg aag ttt tat gat gaa aac aca agg cag tgg tgg atg ccg	2740
Arg Lys Val Lys Phe Tyr Asp Glu Asn Thr Arg Gln Trp Trp Met Pro	
735 740 745	

gat acc gga gga gct aac atc cca gct ctg aat gag ctg ctg tct gtg	2788
Asp Thr Gly Gly Ala Asn Ile Pro Ala Leu Asn Glu Leu Leu Ser Val	
750 755 760	
tggt aac atg ggg ttc agc gat ggc ctg tat gaa ggg gag ttc acc ctg	2836
Trp Asn Met Gly Phe Ser Asp Gly Leu Tyr Glu Gly Glu Phe Thr Leu	
765 770 775 780	
gcc aac cat gac atg tat tat gcg tca ggg tgc agc atc gcg aag ttt	2884
Ala Asn His Asp Met Tyr Tyr Ala Ser Gly Cys Ser Ile Ala Lys Phe	
785 790 795	
cca gaa gat ggc gtc gtg ata aca cag act ttc aag gac caa gga ttg	2932
Pro Glu Asp Gly Val Val Ile Thr Gln Thr Phe Lys Asp Gln Gly Leu	
800 805 810	
gag gtt tta aag cag gaa aca gca gtt gtt gaa aac gtc ccc att ttg	2980
Glu Val Leu Lys Gln Glu Thr Ala Val Val Glu Asn Val Pro Ile Leu	
815 820 825	
gga ctt tat cag att cca gct gag ggt gga ggc cgg att gta ctg tat	3028
Gly Leu Tyr Gln Ile Pro Ala Glu Gly Gly Gly Arg Ile Val Leu Tyr	
830 835 840	
ggg gac tcc aat tgc ttg gat gac agt cac cga cag aag gac tgc ttt	3076
Gly Asp Ser Asn Cys Leu Asp Asp Ser His Arg Gln Lys Asp Cys Phe	
845 850 855 860	
tggt ctt ctg gat gcc ctc ctc cag tac aca tcg tat ggg gtg aca ccg	3124
Trp Leu Leu Asp Ala Leu Leu Gln Tyr Thr Ser Tyr Gly Val Thr Pro	
865 870 875	
cct agc ctc agt cac tct ggg aac cgc cag cgc cct ccc agt gga gca	3172
Pro Ser Leu Ser His Ser Gly Asn Arg Gln Arg Pro Pro Ser Gly Ala	
880 885 890	
ggc tca gtc act cca gag agg atg gaa gga aac cat ctt cat cgg tac	3220
Gly Ser Val Thr Pro Glu Arg Met Glu Gly Asn His Leu His Arg Tyr	
895 900 905	
tcc aag gtt ctg gag gcc cat ttg gga gac cca aaa cct cgg cct cta	3268
Ser Lys Val Leu Glu Ala His Leu Gly Asp Pro Lys Pro Arg Pro Leu	
910 915 920	
cca gcc tgt cca cgc ttg tct tgg gcc aag cca cag cct tta aac gag	3316
Pro Ala Cys Pro Arg Leu Ser Trp Ala Lys Pro Gln Pro Leu Asn Glu	
925 930 935 940	

acg gcg ccc agt aac ctt tgg aaa cat cag aag cta ctc tcc att gac 3364
 Thr Ala Pro Ser Asn Leu Trp Lys His Gln Lys Leu Leu Ser Ile Asp
 945 950 955

ctg gac aag gtg gtg tta ccc aac ttt cga tgc aat cgc cct caa gtg 3412
 Leu Asp Lys Val Val Leu Pro Asn Phe Arg Ser Asn Arg Pro Gln Val
 960 965 970

agg ccc ttg tcc cct gga gag agc ggc gcc tgg gac att cct gga ggg 3460
 Arg Pro Leu Ser Pro Gly Glu Ser Gly Ala Trp Asp Ile Pro Gly Gly
 975 980 985

atc atg cct ggc cgc tac aac cag gag gtg ggc cag acc att cct gtc 3508
 Ile Met Pro Gly Arg Tyr Asn Gln Glu Val Gly Gln Thr Ile Pro Val
 990 995 1000

ttt gcc ttc ctg gga gcc atg gtg gtc ctg gcc ttc ttt gtg gta caa 3556
 Phe Ala Phe Leu Gly Ala Met Val Val Leu Ala Phe Phe Val Val Gln
 1005 1010 1015 1020

atc aac aag gcc aag agc agg ccg aag cgg agg aag ccc agg gtg aag 3604
 Ile Asn Lys Ala Lys Ser Arg Pro Lys Arg Arg Lys Pro Arg Val Lys
 1025 1030 1035

cgc ccg cag ctc atg cag cag gtt cac ccg cca aag acc cct tgc gtg 3652
 Arg Pro Gln Leu Met Gln Gln Val His Pro Pro Lys Thr Pro Ser Val
 1040 1045 1050

tgaccggcag cctggctgac cgtgagggcc agagagagcc ttcacggacg gcgctggtgg 3712

gtgagccgag ctgtggtggc ggctgggttta aaagggatcc agtttcacgc tgcagggtttg 3772

ttagagtctg ttctacatgg gctgcccctc ctgtgatggg cagaggctcc tggtagatcg 3832

agaagattcc tgtggatccc gtcaggaggg acttagtggc tctgccgcca gtgagacttc 3892

ccgccggcag ctgtgcgcac caaagactcg ggagaactgg aaaggctgtc tggggctctc 3952

tgactgcagg ggaaggatgt actttccaaa caaatgatac aaccctgacc aagctaaaag 4012

acgcttggtta aaggctatatt tctatatatta ttgttgggaa aagtcacttt aaagacttgt 4072

gctatttgga agcaaagcta ttttttttgt cagtggaaatg cagttttttt actattccat 4132

catgaggaac aacatagatt ccatgatctt tttaatgaca gtacagactg agatttgaag 4192

gaaacatgca caaatctgta aaacatagac cttcgcttta tttttgtaag tatcacctgc 4252

caccatgttt tgtaatttga ggtcttgatt tcaccattgt cggatgaagaa aattttcaat 4312

aaatatgtat tacccgtctg aagctt

4338

<210> 6

<211> 1052

<212> PRT

<213> Homo sapiens

<400> 6

Met Lys Leu Val Asn Ile Trp Leu Leu Leu Leu Val Val Leu Leu Cys
1 5 10 15

Gly Lys Lys His Leu Gly Asp Arg Leu Glu Lys Lys Ser Phe Glu Lys
20 25 30

Ala Pro Cys Pro Gly Cys Ser His Leu Thr Leu Lys Val Glu Phe Ser
35 40 45

Ser Thr Val Val Glu Tyr Glu Tyr Ile Val Ala Phe Asn Gly Tyr Phe
50 55 60

Thr Ala Lys Ala Arg Asn Ser Phe Ile Ser Ser Ala Leu Lys Ser Ser
65 70 75 80

Glu Val Asp Asn Trp Arg Ile Ile Pro Arg Asn Asn Pro Ser Ser Asp
85 90 95

Tyr Pro Ser Asp Phe Glu Val Ile Gln Ile Lys Glu Lys Gln Lys Ala
100 105 110

Gly Leu Leu Thr Leu Glu Asp His Pro Asn Ile Lys Arg Val Thr Pro
115 120 125

Gln Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp Pro Thr
130 135 140

Val Pro Cys Asn Glu Thr Arg Trp Ser Gln Lys Trp Gln Ser Ser Arg
145 150 155 160

Pro Leu Arg Arg Ala Ser Leu Ser Leu Gly Ser Gly Phe Trp His Ala
165 170 175

Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Pro Arg Gln
180 185 190

Val Ala Gln Thr Leu Gln Ala Asp Val Leu Trp Gln Met Gly Tyr Thr

195	200	205
Gly Ala Asn Val Arg Val Ala Val Phe Asp Thr Gly Leu Ser Glu Lys		
210	215	220
His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn Trp Thr Asn Glu		
225	230	235 240
Arg Thr Leu Asp Asp Gly Leu Gly His Gly Thr Phe Val Ala Gly Val		
	245	250 255
Ile Ala Ser Met Arg Glu Cys Gln Gly Phe Ala Pro Asp Ala Glu Leu		
	260	265 270
His Ile Phe Arg Val Phe Thr Asn Asn Gln Val Ser Tyr Thr Ser Trp		
	275	280 285
Phe Leu Asp Ala Phe Asn Tyr Ala Ile Leu Lys Lys Ile Asp Val Leu		
	290	295 300
Asn Leu Ser Ile Gly Gly Pro Asp Phe Met Asp His Pro Phe Val Asp		
305	310	315 320
Lys Val Trp Glu Leu Thr Ala Asn Asn Val Ile Met Val Ser Ala Ile		
	325	330 335
Gly Asn Asp Gly Pro Leu Tyr Gly Thr Leu Asn Asn Pro Ala Asp Gln		
	340	345 350
Met Asp Val Ile Gly Val Gly Gly Ile Asp Phe Glu Asp Asn Ile Ala		
	355	360 365
Arg Phe Ser Ser Arg Gly Met Thr Thr Trp Glu Leu Pro Gly Gly Tyr		
	370	375 380
Gly Arg Met Lys Pro Asp Ile Val Thr Tyr Gly Ala Gly Val Arg Gly		
385	390	395 400
Ser Gly Val Lys Gly Gly Cys Arg Ala Leu Ser Gly Thr Ser Val Ala		
	405	410 415
Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val Ser Thr Val Gln		
	420	425 430
Lys Arg Glu Leu Val Asn Pro Ala Ser Met Lys Gln Ala Leu Ile Ala		
	435	440 445
Ser Ala Arg Arg Leu Pro Gly Val Asn Met Phe Glu Gln Gly His Gly		

705		710		715		720
Val Ile Phe Ser Asp Trp Tyr Asn Thr Ser Val Met Arg Lys Val Lys						
	725			730		735
Phe Tyr Asp Glu Asn Thr Arg Gln Trp Trp Met Pro Asp Thr Gly Gly						
	740			745		750
Ala Asn Ile Pro Ala Leu Asn Glu Leu Leu Ser Val Trp Asn Met Gly						
	755			760		765
Phe Ser Asp Gly Leu Tyr Glu Gly Glu Phe Thr Leu Ala Asn His Asp						
	770			775		780
Met Tyr Tyr Ala Ser Gly Cys Ser Ile Ala Lys Phe Pro Glu Asp Gly						
	785			790		800
Val Val Ile Thr Gln Thr Phe Lys Asp Gln Gly Leu Glu Val Leu Lys						
	805			810		815
Gln Glu Thr Ala Val Val Glu Asn Val Pro Ile Leu Gly Leu Tyr Gln						
	820			825		830
Ile Pro Ala Glu Gly Gly Gly Arg Ile Val Leu Tyr Gly Asp Ser Asn						
	835			840		845
Cys Leu Asp Asp Ser His Arg Gln Lys Asp Cys Phe Trp Leu Leu Asp						
	850			855		860
Ala Leu Leu Gln Tyr Thr Ser Tyr Gly Val Thr Pro Pro Ser Leu Ser						
	865			870		875
His Ser Gly Asn Arg Gln Arg Pro Pro Ser Gly Ala Gly Ser Val Thr						
	885			890		895
Pro Glu Arg Met Glu Gly Asn His Leu His Arg Tyr Ser Lys Val Leu						
	900			905		910
Glu Ala His Leu Gly Asp Pro Lys Pro Arg Pro Leu Pro Ala Cys Pro						
	915			920		925
Arg Leu Ser Trp Ala Lys Pro Gln Pro Leu Asn Glu Thr Ala Pro Ser						
	930			935		940
Asn Leu Trp Lys His Gln Lys Leu Leu Ser Ile Asp Leu Asp Lys Val						
	945			950		955
						960
Val Leu Pro Asn Phe Arg Ser Asn Arg Pro Gln Val Arg Pro Leu Ser						

965	970	975
Pro Gly Glu Ser Gly Ala Trp Asp Ile Pro Gly Gly Ile Met Pro Gly		
980	985	990
Arg Tyr Asn Gln Glu Val Gly Gln Thr Ile Pro Val Phe Ala Phe Leu		
995	1000	1005
Gly Ala Met Val Val Leu Ala Phe Phe Val Val Gln Ile Asn Lys Ala		
1010	1015	1020
Lys Ser Arg Pro Lys Arg Arg Lys Pro Arg Val Lys Arg Pro Gln Leu		
025	1030	1040
Met Gln Gln Val His Pro Pro Lys Thr Pro Ser Val		
1045	1050	

<210> 7
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Peptide

<220>
 <221> MOD_RES
 <222> (2)
 <223> Xaa represents any amino acid.

<220>
 <221> MOD_RES
 <222> (3)
 <223> Xaa represents an alkyl or an aromatic hydrophobic amino acid.

<220>
 <221> MOD_RES
 <222> (4)..(6)
 <223> Xaa represents any amino acid.

<220>
 <221> MOD_RES
 <222> (7)
 <223> Xaa represents an acidic amino acid.

<400> 7

Arg Xaa Xaa Xaa Xaa Xaa Xaa

1

5

<210> 8

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<220>

<221> MOD_RES

<222> (2)

<223> Xaa represents any amino acid.

<220>

<221> MOD_RES

<222> (3)

<223> Xaa represents an alkyl or an aromatic hydrophobic amino acid.

<220>

<221> MOD_RES

<222> (4)

<223> Xaa represents Lys, Leu, Phe or Thr.

<220>

<221> MOD_RES

<222> (5)..(6)

<223> Xaa represents any amino acid.

<220>

<221> MOD_RES

<222> (7)

<223> Xaa represents an acidic amino acid.

<400> 8

Arg Xaa Xaa Xaa Xaa Xaa Xaa

1

5

<210> 9

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<220>

<221> MOD_RES

<222> (2)

<223> Xaa represents any amino acid.

<220>

<221> MOD_RES

<222> (3)

<223> Xaa represents an alkyl or an aromatic hydrophobic acid.

<220>

<221> MOD_RES

<222> (4)..(7)

<223> Xaa represents any amino acid.

<220>

<221> MOD_RES

<222> (8)

<223> Xaa represents an acidic amino acid.

<400> 9

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1

5

<210> 10

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<220>

<221> MOD_RES

<222> (2)

<223> Xaa represents any amino acid.

<220>

<221> MOD_RES

<222> (3)

<223> Xaa represents an alkyl or an aromatic hydrophobic amino acid.

<220>
<221> MOD_RES
<222> (4)
<223> Xaa represents Lys, Leu, Phe or Thr.

<220>
<221> MOD_RES
<222> (5)..(7)
<223> Xaa represents any amino acid.

<220>
<221> MOD_RES
<222> (8)
<223> Xaa represents an acidic amino acid.

<400> 10
Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 11
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<220>
<221> MOD_RES
<222> (2)
<223> Xaa represents any amino acid.

<220>
<221> MOD_RES
<222> (3)
<223> Xaa is an alkyl or an aromatic hydrophobic amino acid.

<220>
<221> MOD_RES
<222> (4)..(8)
<223> Xaa represents any amino acid.

<220>
<221> MOD_RES
<222> (9)

<223> Xaa represents an acidic amino acid.

<400> 11

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

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<210> 12

<211> 9

<212> PRT

<213> Artificial Sequence

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<220>

<221> MOD_RES

<222> (2)

<223> Xaa represents any amino acid.

<220>

<221> MOD_RES

<222> (3)

<223> Xaa represents an alkyl or an aromatic hydrophobic amino acid.

<220>

<221> MOD_RES

<222> (4)

<223> Xaa represents Lys, Leu, Phe or Thr.

<220>

<221> MOD_RES

<222> (5)..(8)

<223> Xaa represents any amino acid.

<220>

<221> MOD_RES

<222> (9)

<223> Xaa represents an acid amino acid.

<400> 12

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1

5

<210> 13

<211> 11

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Peptide

 <400> 13
 Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp
 1 5 10

 <210> 14
 <211> 13
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Peptide

 <220>
 <221> MOD_RES
 <222> (1)
 <223> Xaa represents orthoaminobenzoic acid.

 <220>
 <221> MOD_RES
 <222> (13)
 <223> Xaa represents 3-nitrotyrosine.

 <400> 14
 Xaa Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp Xaa
 1 5 10

 <210> 15
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
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 <220>
 <221> modified_base
 <222> (3)
 <223> i

<220>
<221> modified_base
<222> (9)
<223> i

<220>
<221> modified_base
<222> (12)
<223> i

<220>
<221> modified_base
<222> (18)
<223> i

<220>
<221> modified_base
<222> (21)
<223> i

<400> 15
ggncayggna cnywykngc ngg

23

<210> 16
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<220>
<221> modified_base
<222> (3)
<223> i

<220>
<221> modified_base
<222> (6)
<223> i

<220>
<221> modified_base
<222> (9)
<223> i

<220>
<221> modified_base
<222> (12)
<223> i

<220>
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<222> (15)
<223> i

<220>
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<222> (18)
<223> i

<220>
<221> modified_base
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<223> i

<220>
<221> modified_base
<222> (24)
<223> i

<220>
<221> modified_base
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<223> i

<400> 16
ccngynacnw snggnswngc nacnswgtnc c

31

<210> 17
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<220>
<221> MOD_RES
<222> (5)
<223> Xaa represents histidine or phenylalanine.

<220>

<221> MOD_RES
<222> (6)
<223> Xaa represents valine or cysteine.

<400> 17
Gly His Gly Thr Xaa Xaa Ala Gly
1 5

<210> 18
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<220>
<221> MOD_RES
<222> (4)
<223> Xaa represents valine or methionine.

<220>
<221> MOD_RES
<222> (6)
<223> Xaa represents threonine or serine.

<220>
<221> MOD_RES
<222> (8)
<223> Xaa represents histidine or valine.

<220>
<221> MOD_RES
<222> (10)
<223> Xaa represents alanine or threonine.

<400> 18
Gly Thr Ser Xaa Ala Xaa Pro Xaa Val Xaa Gly
1 5 10

<210> 19
<211> 28
<212> DNA
<213> Homo sapiens

<400> 19

ggatccgaag aaacatctgg gcgacaga

28

<210> 20

<211> 24

<212> DNA

<213> Homo sapiens

<400> 20

ctcgagggt ctcagccgtg tgct

24

<210> 21

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 21

gaggaagaga cagggataaa c

21

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 22

gggatatgct tagcattgac

20

<210> 23

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 23

agccctatta cctgaacctg

20

<210> 24

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 24

gaatctgaaa gaactccccc

20

<210> 25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 25

ttccgagatt ccacccctacg

20

<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 26

tgcagctcag caggtctatg

20

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 27

tctcctccaa cctcaaccac

20

<210> 28

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 28

ccagcctgtc atcctcaata tc

22

<210> 29

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 29

ggagccatgg attgcacttt c

21

<210> 30

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide

<400> 30

aggagctcaa tgtggcagga

20

<210> 31

<211> 27

<212> DNA
 <213> Homo sapiens

 <400> 31
 gtgaccatga agcttgtcaa catctgg 27

 <210> 32
 <211> 26
 <212> DNA
 <213> Homo sapiens

 <400> 32
 acactgggtcc ctgagagggc ccggca 26

 <210> 33
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ctcgagtgtc tgggcaacct ggcgcggg

28

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<212> PRT

<213> Homo sapiens

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Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe

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<210> 38

<211> 27

<212> PRT

<213> Homo sapiens

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Gly Gly Ala His Asp Ser Asp Gln His Pro His Ser Gly Ser Gly Arg

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Ser Val Leu Ser Phe Glu Ser Gly Ser Gly Gly

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<210> 39

<211> 18

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<213> Homo sapiens

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Trp His Ala Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile

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Pro Arg

<210> 40

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<212> PRT

<213> Artificial Sequence

<220>

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Glu

<210> 41

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<400> 41

Ser Arg Arg Leu Leu Arg Ala Leu Glu
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<210> 42

<211> 17

<212> PRT

<213> Homo sapiens

<400> 42

Trp Gln Ser Ser Arg Pro Leu Arg Arg Ala Ser Leu Ser Leu Gly Ser
1 5 10 15

Gly

<210> 43

<211> 15

<212> PRT

<213> Homo sapiens

<400> 43

Arg Ala Ile Pro Arg Gln Val Ala Gln Thr Leu Gln Ala Asp Val
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<210> 44

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<212> PRT

<213> Homo sapiens

<400> 44

Pro Gln Arg Lys Val Phe Arg Ser Leu

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<210> 45

<211> 15

<212> PRT

<213> Homo sapiens

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Pro Gln Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp

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15

<210> 46

<211> 14

<212> PRT

<213> Artificial Sequence

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<222> (1)

<223> Xaa represents orthoaminobenzoic acid.

<220>

<221> MOD_RES

<222> (13)

<223> Xaa represents 3-nitrotyrosine.

<220>

<223> Description of Artificial Sequence: Peptide

<400> 46

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<210> 47

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

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<222> (1)

<223> Xaa represents orthoaminobenzoic acid.

<220>
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<223> Xaa represent 3-nitrotyrosine.

<220>
<223> Description of Artificial Sequence: Peptide

<400> 47
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<211> 16
<212> PRT
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Lys Ala Gly Ser Arg Gly Leu Thr Thr Thr Ser Leu Ala Asp Thr Phe
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Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp Pro Thr Val
1 5 10 15

<210> 52

<211> 16

<212> PRT

<213> Homo sapiens

<400> 52

Thr Pro Gln Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp
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<210> 53

<211> 16

<212> PRT

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<400> 53

Val Thr Pro Gln Arg Lys Val Phe Arg Ser Leu Lys Lys Tyr Ala Glu
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<400> 54

Ser Gly Ser Gly Arg Ser Val Leu Ser Phe Glu Ser Gly Ser Gly Gly
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<211> 16

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<400> 55

His Ser Pro Gly Arg Asn Val Leu Gly Thr Glu Ser Arg Asp Gly Pro
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<210> 56

<211> 16

<212> PRT
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<400> 56
Ala Ser Val Gly Arg Leu Ala Leu Ser Gln Glu Glu Pro Ala Pro Leu
1 5 10 15

<210> 57
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<212> PRT
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<400> 57
Arg Ile Ser Asp Arg Asp Tyr Met Gly Trp Met Asp Phe Gly Arg Arg
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<210> 58
<211> 16
<212> PRT
<213> Rattus sp.

<400> 58
Asp Pro Arg Leu Arg Gln Phe Leu Gln Lys Ser Leu Ala Ala Ala Thr
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<210> 59
<211> 16
<212> PRT
<213> Bovis sp.

<400> 59
Leu Leu Lys Glu Leu Gln Asp Leu Ala Leu Gln Gly Ala Lys Glu Arg
1 5 10 15

<210> 60
<211> 16
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<213> Bovis sp.

<400> 60
Met Ala Arg Ala Pro Gln Val Leu Phe Arg Gly Gly Lys Ser Gly Glu
1 5 10 15

<210> 61
<211> 16
<212> PRT
<213> Bovis sp.

<400> 61
Glu Leu Glu Asn Leu Ala Ala Met Asp Leu Glu Leu Gln Lys Ile Ala
1 5 10 15

<210> 62
<211> 16
<212> PRT
<213> Bovis sp.

<400> 62
Ala Ala Met Asp Leu Glu Leu Gln Lys Ile Ala Glu Lys Phe Ser Gly
1 5 10 15

<210> 63
<211> 16
<212> PRT
<213> Rattus sp.

<400> 63
Lys Ser Ser Phe Thr Asn Val Thr Ser Pro Val Val Leu Thr Asn Tyr
1 5 10 15

<210> 64
<211> 16
<212> PRT
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<400> 64
Lys Ser Gln Thr Pro Leu Val Thr Leu Phe Lys Asn Ala Ile Ile Lys
1 5 10 15

<210> 65
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<212> PRT
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<400> 65
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<400> 66
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<210> 67
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<400> 67
Leu Leu Arg Lys Lys Arg Thr Thr Ser Ala Glu Lys Asn Thr Cys Gln
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<210> 68
<211> 16
<212> PRT
<213> Homo sapiens

<400> 68
Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser
1 5 10 15

<210> 69
<211> 16
<212> PRT
<213> Homo sapiens

<400> 69
Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser
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<210> 70
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Ile Ser Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr
1 5 10 15

<210> 71
<211> 16
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<400> 71
Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val
1 5 10 15

<210> 72
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 72
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1 5 10

<210> 73
<211> 12
<212> PRT
<213> Homo sapiens

<400> 73
Ser Gly Ser Gly Arg Ser Val Leu Ser Phe Glu Ser
1 5 10

<210> 74
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<220>

<221> MOD_RES
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 <223> Xaa represents 3-nitrotyrosine.

 <220>
 <223> Description of Artificial Sequence: Peptide

 <400> 74
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<210> 75
 <211> 12
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<220>
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<220>
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 <223> Xaa represents orthoaminobenzoic acid.

<220>
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 <223> Xaa represents 3-nitrotyrosine.

<400> 75
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<210> 76
 <211> 15
 <212> PRT
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<220>
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<220>
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<223> Xaa represents 3-nitrotyrosine.

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<223> Description of Artificial Sequence: Peptide

<400> 76

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